

WHAT IS CLAIMED IS:

1 1. A purified nucleic acid molecule, comprising a  
2 nucleic acid sequence encoding SEQ ID NO.: 2.

1 2. The purified nucleic acid molecule of claim 1,  
2 which is a cDNA molecule.

1 3. The purified nucleic acid molecule of claim 2,  
2 which comprises the sequence of SEQ ID NO.: 1.

1 4. A purified nucleic acid, wherein said nucleic acid  
2 is capable of hybridizing at high stringency to a probe of  
3 400 contiguous nucleotides from SEQ ID NO.: 1 over the entire  
4 length of said probe.

1 5. A purified nucleic acid, comprising a sequence that  
2 encodes a protein that is at least 90% homologous to the  
3 entire length of amino acid sequence of SEQ ID NO.: 2.

1           6.    The purified nucleic acid of claim 5, wherein the  
2   protein is at least 95% homologous to SEQ ID NO.: 2.

1           7.    The purified nucleic acid of claim 5, wherein the  
2   protein is at least 98% homologous to SEQ ID NO.: 2.

1           8.    A purified protein, comprising a sequence that is  
2   at least 80% homologous to the entire length of SEQ ID NO.:  
3   2.

1           9.    The purified protein of claim 8, wherein the  
2   sequence is at least 90% homologous to SEQ ID NO.: 2.

1           10.   The purified protein of claim 9, wherein the  
2   sequence is at least 95% homologous to SEQ ID NO.: 2.

1           11.   The purified protein of claim 9, wherein the  
2   sequence is at least 98% homologous to SEQ ID NO.: 2.

1           12.   The purified protein of claim 9, wherein the  
2   sequence is SEQ ID NO.: 2.

1           13. A method for targeting gene sequences having one  
2 or more phenotypic characteristics using a computer, the  
3 method comprising the steps of:  
4           selecting one or more phenotypic characteristics;  
5           selecting a gene sequence that is known to have the  
6 selected phenotypic characteristics;  
7           selecting one or more databases containing  
8 cataloged gene sequences;  
9           comparing the selected gene sequence to the  
10 cataloged gene sequences;  
11           extracting any cataloged gene sequences that  
12 contain a portion of the selected gene sequence;  
13           aligning the selected gene sequence to each portion  
14 of the extracted gene sequence;  
15           prioritizing the extracted gene sequences based on  
16 the alignment of the selected gene sequence;  
17           selecting at least one of the prioritized gene  
18 sequences based on one or more phenotypic criteria; and  
19           designing one or more degenerate primers to target  
20 the selected-prioritized gene sequences.

1 14. The method as recited in claim 13, further  
2 comprising the step of filtering the prioritized gene  
3 sequences.

1 15. The method as recited in claim 14, wherein the step  
2 of filtering the prioritized gene sequences removes  
3 vertebrate sequences but not invertebrate derived sequences.

1 16. The method as recited in claim 13, further  
2 comprising the step of cloning genetic material using the one  
3 or more degenerate primers.

1 17. The method as recited in claim 13, wherein the one  
2 or more databases are selected from cataloged gene sequences  
3 for humans, rats, mice, zebra fish, frogs, Drosophila,  
4 nematode, C. elegans, mosquito and bacteria.

1 18. The method as recited in claim 13, wherein the  
2 phenotypic characteristics include insect mid-gut epithelial  
3 cell encoded proteins.

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19. The method as recited in claim 13, wherein the one  
or more degenerate primers are nested.

20. The method as recited in claim 13, wherein the one  
or more degenerate primers is used to clone target molecules.

21. The method as recited in claim 13, wherein the one  
or more degenerate primers is used to clone biopesticide  
encoding genes.

22. The method as recited in claim 13, wherein the one  
or more degenerate primers is used to clone therapeutic  
encoding genes.

23. The method as recited in claim 13, wherein the step  
of prioritizing the extracted gene sequences based on the  
alignment of the selected gene sequence is accomplished by  
using a statistical analysis of the alignment.

24. The method as recited in claim 13, wherein the step  
of aligning the selected gene sequences to each extracted

3 gene sequence ~~is~~ accomplished using a local alignment search  
4 tool.

1 25. The method as recited in claim 13, wherein the  
2 selected gene sequence is aligned to each extracted gene  
3 sequence by amino acid sequences.

1 26. The method as recited in claim 13, wherein the  
2 selected gene sequence is aligned to each extracted gene  
3 sequence by nucleic acid sequences.

1 27. The method as recited in claim 13, wherein the  
2 selected gene sequence is aligned to each extracted gene  
3 sequence by genomic DNA.

1 28. The method as recited in claim 13, wherein the  
2 selected gene sequence is aligned to each extracted gene  
3 sequence by open reading frames.

1 29. The method as recited in claim 13, wherein the  
2 selected gene sequence is aligned to each extracted gene  
3 sequence by introns.

1           30. The method as recited in claim 13, wherein the  
2           selected gene sequence is aligned to each extracted gene  
3           sequence by introns and exons.

1           31. The method as recited in claim 13, wherein the one  
2           or more phenotypic criteria excludes genes encoded by  
3           mammals.

1           32. The method as recited in claim 13, wherein the one  
2           or more phenotypic criteria excludes genes encoded by zebra  
3           fish or frogs.

1           33. The method as recited in claim 13, wherein the one  
2           or more phenotypic criteria excludes genes encoded by  
3           invertebrates.

1           34. A system for targeting gene sequences having one  
2           or more characteristics comprising:

3           a computer having program means thereon for selecting  
4           one or more phenotypic characteristics, selecting a gene  
5           sequence that is known to have the selected phenotypic  
6           characteristics, comparing the selected gene sequence to the  
7           cataloged gene sequences, extracting any cataloged gene

8 sequences that contain a portion of the selected gene  
9 sequence, aligning the selected gene sequence to each portion  
10 of the extracted gene sequence, prioritizing the extracted  
11 gene sequences based on the alignment of the selected gene  
12 sequence, selecting at least one of the prioritized gene  
13 sequences based on one or more phenotypic criteria, and  
14 designing one or more degenerate primers to target the  
15 selected-prioritized gene sequences;

16 one or more databases containing the cataloged gene  
17 sequences; and

18 a communication link connecting the computer to said one  
19 or more databases.

1 35. The system as recited in claim 34, further  
2 comprising:

3 at least one other computer, connected to said computer,  
4 said at least one other computer having said program means  
5 thereon for selecting one or more phenotypic characteristics,  
6 selecting a gene sequence that is known to have the selected  
7 phenotypic characteristics, comparing the selected gene  
8 sequence to the cataloged gene sequences, extracting any  
9 cataloged gene sequences that contain a portion of the  
10 selected gene sequence, aligning the selected gene sequence

11 to each portion of the extracted gene sequence, prioritizing  
12 the extracted gene sequences based on the alignment of the  
13 selected gene sequence, selecting at least one of the  
14 prioritized gene sequences based on one or more phenotypic  
15 criteria, and designing one or more degenerate primers to  
16 target the selected-prioritized gene sequences.

1 36. The system as recited in claim 34 or 35, wherein  
2 the program means on said computer filters the prioritized  
3 gene sequences.

1 37. The system as recited in claim 36, wherein the  
2 program means on said computer removes vertebrate sequences  
3 but not invertebrate derived sequences when the prioritized  
4 sequences are filtered.

1 38. The system as recited in claim 36, further  
2 comprising an apparatus that clones genetic material using  
3 one or more degenerate primers.

1 39. The system as recited in claim 36, wherein the one  
2 or more databases are selected from cataloged gene sequences

3 for humans, rats, mice, zebra fish, frogs, Drosophila,  
4 nematode, C. elegans, mosquito and bacteria.

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2 40. The system as recited in claim 36, wherein the  
3 phenotypic characteristics include insect mid-gut epithelial  
cell encoded proteins.

1 41. The system as recited in claim 36, wherein the one  
2 or more degenerate primers are nested.

1 42. The system as recited in claim 36, wherein the one  
2 or more degenerate primers is used to clone target molecules.

1 43. The system as recited in claim 36, wherein the one  
2 or more degenerate primers is used to clone biopesticide  
3 encoding genes.

1 44. The system as recited in claim 36, wherein the one  
2 or more degenerate primers is used to clone therapeutic  
3 encoding genes.

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1 45. The system as recited in claim 36, wherein the  
2 program means on said computer uses a statistical analysis

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3 of the alignment of the selected gene sequence to prioritize  
4 the extracted gene sequences.

1 46. The system as recited in claim 36, wherein the  
2 program means on said computer uses a local alignment search  
3 tool to align the selected gene sequence to each extracted  
4 gene sequence.

1 47. The system as recited in claim 36, wherein the  
2 selected gene sequence is aligned to each extracted gene  
3 sequence by amino acid sequences.

1 48. The system as recited in claim 36, wherein the  
2 selected gene sequence is aligned to each extracted gene  
3 sequence by nucleic acid sequences.

1 49. The system as recited in claim 36, wherein the  
2 selected gene sequence is aligned to each extracted gene  
3 sequence by genomic DNA.

1 50. The system as recited in claim 36, wherein the  
2 selected gene sequence is aligned to each extracted gene  
3 sequence by open reading frames.

1           51. The system as recited in claim 36, wherein the  
2           selected gene sequence is aligned to each extracted gene  
3           sequence by introns.

1           52. The system as recited in claim 36, wherein the  
2           selected gene sequence is aligned to each extracted gene  
3           sequence by introns and exons.

1           53. The system as recited in claim 36, wherein the one  
2           or more phenotypic criteria excludes genes encoded by  
3           mammals.

1           54. The system as recited in claim 36, wherein the one  
2           or more phenotypic criteria excludes genes encoded by zebra  
3           fish or frogs.

1           55. The system as recited in claim 36, wherein the one  
2           or more phenotypic criteria excludes genes encoded by  
3           invertebrates.

1           56. The system as recited in claim 36, wherein said  
2           system may be used for high specificity primer selection.

1           58. The system as recited in claim 36, wherein said  
2    system may be used for high throughput database conversion.

59. The system as recited in claim 36, wherein said system may be used for high throughput positioning of motifs.

1           60. A computer program embodied on a computer-readable  
2   medium for targeting gene sequences having one or more  
3   phenotypic characteristics, said computer program comprising:

4 first selecting means for selecting one or more  
5 phenotypic characteristics of said gene sequences;

6       second selecting means for selecting a gene sequence  
7       that is known to have said one or more of said selected  
8       phenotypic characteristics;

9        third selecting means for selecting at least one  
10        database containing cataloged gene sequences therein;

11 extracting means for extracting from said at least one  
12 database a plurality of cataloged gene sequences containing  
13 a portion of the said given gene sequence;

14 aligning means for aligning said given gene sequence to  
15 respective ones of said cataloged gene sequence;

16 prioritizing means for prioritizing the respective ones  
17 of the extracted gene sequences based on the alignment of the  
18 given gene sequence;

19 fourth selecting means for selecting at least one of the  
20 prioritized gene sequences based on one or more phenotypic  
21 criteria; and

22 designing means for designing one or more degenerate  
23 primers to target said at least one selected gene sequence.

1 61. The computer program as recited in claim 60,  
2 further comprising a code segment for filtering the  
3 prioritized gene sequences.

1 62. The computer program as recited in claim 61,  
2 wherein the code segment for filtering the prioritized gene  
3 sequences removes vertebrate sequences but not invertebrate  
4 derived sequences.

1 63. The computer program as recited in claim 60,  
2 further comprising a code segment for cloning genetic  
3 material using the one or more degenerate primers.

1           64. The computer program as recited in claim 60,  
2 wherein the one or more databases are selected from cataloged  
3 gene sequences for humans, rats, mice, zebra fish, frogs,  
4 Drosophila, nematode, C. elegans, mosquito and bacteria.

1           65. The computer program as recited in claim 60,  
2 wherein the phenotypic characteristics include insect mid-gut  
3 epithelial cell encoded proteins.

1           66. The computer program as recited in claim 60,  
2 wherein the one or more degenerate primers are nested.

1           67. The computer program as recited in claim 60,  
2 wherein the one or more degenerate primers is used to clone  
3 target molecules.

1           68. The computer program as recited in claim 60,  
2 wherein the one or more degenerate primers is used to clone  
3 biopesticide encoding genes.

1           69. The computer program as recited in claim 60,  
2           wherein the one or more degenerate primers is used to clone  
3           therapeutic encoding genes.

1           70. The computer program as recited in claim 60,  
2           wherein the code segment for prioritizing the extracted gene  
3           sequences based on alignment of the selected gene is  
4           accomplished by using a statistical analysis of the  
5           alignment.

1           71. The computer program as recited in claim 60,  
2           wherein the code segment for prioritizing the extracted gene  
3           sequences based on alignment of the selected gene is  
4           accomplished by using a local alignment search tool.

1           72. The computer program as recited in claim 60,  
2           wherein the selected gene sequence is aligned to each  
3           extracted gene sequence by amino acid sequences.

1           73. The computer program as recited in claim 60,  
2           wherein the selected gene sequence is aligned to each  
3           extracted gene sequence by nucleic acid sequences.

1           74. The computer program as recited in claim 60,  
2           wherein the selected gene sequence is aligned to each  
3           extracted gene sequence by genomic DNA.

1           75. The computer program as recited in claim 60,  
2           wherein the selected gene sequence is aligned to each  
3           extracted gene sequence by open reading frames.

1           76. The computer program as recited in claim 60,  
2           wherein the selected gene sequence is aligned to each  
3           extracted gene sequence by introns.

1           77. The computer program as recited in claim 60,  
2           wherein the selected gene sequence is aligned to each  
3           extracted gene sequence by introns and exons.

1           78. The computer program as recited in claim 60,  
2           wherein the one or more phenotypic criteria excludes genes  
3           encoded by mammals.

1           79. The computer program as recited in claim 60,  
2           wherein the one or more phenotypic criteria excludes genes  
3           encoded by zebra fish or frogs.

1           80. The computer program as recited in claim 60,  
2           wherein the one or more phenotypic criteria excludes genes  
3           encoded by invertebrates.

1           81. An article of manufacture comprising a computer  
2           usable medium having computer readable program code means  
3           embodied therein for targeting gene sequences, the computer  
4           readable program code means in said article of manufacture  
5           comprising:

6           computer readable code means for selecting one or more  
7           phenotypic characteristics;

8           computer readable code means for selecting a gene  
9           sequence that is known to have the selected phenotypic  
10          characteristics;

11          computer readable code means for selecting one or more  
12          databases containing cataloged gene sequences;

13          computer readable code means for comparing the selected  
14          gene sequence to the cataloged gene sequences;

15          computer readable code means for extracting any  
16          cataloged gene sequences that contain a portion of the  
17          selected gene sequence;

18 computer readable code means for aligning the selected  
19 gene sequence to each portion of the extracted gene sequence;  
20 computer readable code means for prioritizing the  
21 extracted gene sequences based on the alignment of the  
22 selected gene sequence;  
23 computer readable code means for selecting at least one  
24 of the prioritized gene sequences based on one or more  
25 phenotypic criteria; and  
26 computer readable code means for designing one or more  
27 degenerate primers to target the selected-prioritized gene  
28 sequences.

1 82. The article of manufacture of claim 81, wherein  
2 said article of manufacture is stored on a medium selected  
3 from a group consisting of:  
4 a server, a hard drive, a CD-ROM and a diskette.